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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.40155 Seconds

(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613B-4

Perfect score: 579  
Sequence: 1 ODMLTFQKKHLLTFTRDVDCN.....TFCVTCENQAPVHFVGSHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	94.5	104	1	RN30_RANPI
2	286	49.4	111	1	RNPO_RANCA
3	279.5	48.3	111	1	LECS_RANCA
4	263.5	45.5	111	1	RNPL_RANCA
5	142	24.5	119	1	RNP_IGUG
6	124.5	21.5	145	1	ANGR_MOUSE
7	124.5	21.5	146	1	ANGI_CERAE
8	123	21.2	124	1	RNP_GALMU
9	120	20.7	148	1	ANGI_BOVIN
10	118	20.4	128	1	RNP_MYOCO
11	117	20.2	124	1	RNP_BALAC
12	116	20.0	146	1	ANGI_MACMU
13	115.5	19.9	145	1	ANGI_MOUSE
14	112.5	19.4	145	1	ANGI_PAPHA
15	112.5	19.4	146	1	RNP_PROGU
16	111	19.2	128	1	ECPP4_MOUSE
17	110.5	19.1	125	1	ANGI_RABIT
18	110	19.0	128	1	RNP_HYDXY
19	110	19.0	146	1	ANGI_MIOTA
20	110	18.7	147	1	RNLA_HUMAN
21	108.5	18.7	150	1	RNP_CHIBR
22	108	18.7	124	1	RNP_BOVIN
23	108	18.7	156	1	ECPP3_MOUSE
24	107	18.5	147	1	ANGI_HUMAN
25	106	18.3	147	1	ANGI_PANTR
26	106	18.3	124	1	RNP_AEPME
27	105	18.1	124	1	RNP_AETAM
28	105	18.1	124	1	RNP_SHEEP
29	105	18.1	124	1	ANGI_PIG
30	104.5	18.0	150	1	RNK6_SAISC
31	104.5	18.0	150	1	RNP_BUBBU
32	104.5	18.0	124	1	
33	104	18.0	124	1	

34	104	18.0	124	1	RNP_CONTA
35	104	18.0	124	1	RNP_GAZPH
36	103	17.8	123	1	ANG2_BOVIN
37	103	17.8	124	1	RNP_GIRCA
38	103	17.8	124	1	RNP_PIG
39	103	17.8	128	1	RNP_HYSCR
40	103	17.8	156	1	RNP_MYOC
41	103	17.8	167	1	RNBR_BOVIN
42	102	17.6	128	1	RNP_HORSE
43	102	17.6	146	1	ANGI_SAGOE
44	101.5	17.5	155	1	ECPI_MOUSE
45	101	17.4	141	1	RNBR_GIRCA

## ALIGNMENTS

RESULT 1  
ID RN30\_RANPI STANDARD: PRT: 104 AA.  
AC P22069;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DE 01-FEB-1995 (Rel. 31, Last annotation update)  
DE P-30 protein (EC 3.1.27.-) (onconase).  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=91093131; PubMed=1985896;  
RA Ardeli W., Mikulski S.M., Shogen K.;  
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";  
RL J. Biol. Chem. 266:245-251(1991).  
RN [2]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=93066156; PubMed=1438177;  
RA Mosimann S.C., Johns K.L., Ardeli W., Mikulski S.M., Shogen K., James M.N.G.;  
RT "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";  
RL Proteins. 14:392-400(1992).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
RX MEDLINE=94166079; PubMed=8120892;  
RA Mosimann S.C., Ardeli W., James M.N.G.;  
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";  
RL J. Mol. Biol. 236:1141-1153(1994).  
CC -I- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.  
CC -I- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PDB: 1ONC; 31-JAN-94.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA. 1.  
DR PRODOM: PD000535; RNaseA: 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; 3d-structure.  
FT MOD\_RES 1  
FT ACT\_SITE 10  
FT ACT\_SITE 31  
FT ACT\_SITE 97  
FT DISULFID 19  
FT DISULFID 68  
FT DISULFID 75  
FT DISULFID 90

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FT DISULFID 87 104
RT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA: 11845 MW: 22A753C2P9E566B4 CRC64:

Query Match 94.5%; Score 547; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.7e-51;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNVLT 60
   1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNVLT 60
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNVLT 60
QY 61 FEFYLSDCNVTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGHC 104
   61 FEFYLSDCNVTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 FEFYLSDCNVTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 2
RNPO_RANCA STANDARD; PRT; 111 AA.
ID RNPO_RANCA
AC P18916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP TISSUE-Egg;
RC MEDLINE=87299649; PubMed=3304421.
RA Titani K., Takio K., Kuwada M., Nitla K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of stallic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237.
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RP CHARACTERIZATION.
RC TISSUE-Egg;
RX MEDLINE=93192604; PubMed=8448385.
RA Nitla K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of stallic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

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RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS
CC MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
CC EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING
CC NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
CC HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A27121; A27121.
DR PDB: 1BC4; 28-OCT-98.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; fnaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.
FT MOO_RRS 1
FT ACT_SITE 10 10 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F5729ECP4 CRC64:

Query Match 49.4%; Score 286; DB 1; Length 111;
Best Local Similarity 48.6%; Pred. No. 9.5e-24;
Matches 54; Conservative 16; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNV 56
   1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNV 56
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPVKAICGIIASKNV 56
QY 57 VLTFFEFYLSDC---NWTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGHC 104
   60 VLTFFEFYLSDC---NWTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGHC 104
DB 60 VLTFFEFYLSDC---NWTSRCKYKLRKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 3
LECS_RANCA STANDARD; PRT; 111 AA.
ID LECS_RANCA
AC P18839:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stallic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE-Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitla K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: JX0120; JX0120.

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DR HSSP; P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA: 1.  
DR Prodom: PD000535; RNaseA: 1.  
DR SMART: SM00092; RNase\_Pc: 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
KW Hydrolyase: Nuclease; Endonuclease; Sialic acid; Lectin.  
FT ACT\_SITE 10 10  
FT ACT\_SITE 35 35  
FT ACT\_SITE 103 103  
FT ACT\_SITE 19 72  
FT DISULFID 34 82  
FT DISULFID 52 97  
FT DISULFID 94 111  
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 48.3%; Score 279.5; DB 1; Length 111;  
Best Local Similarity 44.1%; Pred. No. 4,7e-23;  
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 QDMVTFQKHLTNRDVDCNNILSTNLF---HCKDKNTFYISRPPEYKATCKGIASKN 56  
1 0NMAKFQEKHRTPTNSNTNCTIMDKSIYIVGGCKERTFTISSATTYKATCSGASTNRN 60  
DB 57 VLTFFEFYLSDC---NVTSPCKYKLTSTNTEFCVTCENAPVHFVGVGHC 104  
61 VLTSTFRLNCTIRSATAPRCPYNSRTETNVCVCKENLPIVFAIGRC 111

RESULT 4  
RNP\_LIGUG  
ID RNP\_LIGUG STANDARD; PRT; 111 AA.  
AC P14626;  
DT 01-FEB-1990 (Rel. 14, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease, liver (EC 3.1.27.5).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=90130374; Pubmed=2613682;  
RA Nitta R, Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
RT Okazaki T., Ohgi K., Irie M.;  
RT "Primary structure of a ribonuclease' from bullfrog (Rana catesbeiana)  
RT liver.";  
RL J. Biochem. 106:729-735(1989).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR HSSP; P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA: 1.  
DR Prodom: PD000535; RNaseA: 1.  
DR SMART: SM00092; RNase\_Pc: 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
KW Hydrolyase: Nuclease; Endonuclease.  
FT MOD\_RES 1  
FT ACT\_SITE 10 10  
FT ACT\_SITE 35 35  
FT ACT\_SITE 104 104  
FT ACT\_SITE 19 72  
FT DISULFID 34 82  
FT DISULFID 52 97  
FT DISULFID 94 111  
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 45.5%; Score 263.5; DB 1; Length 111;  
Best Local Similarity 42.3%; Pred. No. 2.3e-21;  
Matches 47; Conservative 19; Mismatches 38; Indels 7; Gaps 2;

QY 1 QDMVTFQKHLTNRDVDCNNILSTNLF---HCKDKNTFYISRPPEYKATCKGIASKN 56  
1 0NMAKFQEKHRTPTNSNTNCTIMDKSIYIVGGCKERTFTISSATTYKATCSGASTNRN 60  
DB 57 VLTFFEFYLSDC---NVTSPCKYKLTSTNTEFCVTCENAPVHFVGVGHC 104  
61 ELSTSTFRLNCTIRSDITPRCPYHPSPDNNKICVCKEOLPIVFAIGRC 111

RESULT 5  
RNP\_LIGUG  
ID RNP\_LIGUG STANDARD; PRT; 119 AA.  
AC P80287;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
OS Iguana iguana (Common Iguana).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
OX NCBI\_TaxID=8517;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=94139745; Pubmed=8307028;  
RA Zhao W., Beintema J.J., Hofsteenge J.;  
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic  
RT ribonuclease.";  
RL Eur. J. Biochem. 219:641-646(1994).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR HSSP; P00656; 1LSO.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA: 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR Prodom: PD000535; RNaseA: 1.  
DR SMART: SM00092; RNase\_Pc: 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
KW Hydrolyase: Nuclease; Endonuclease.  
FT MOD\_RES 1  
FT DISULFID 25 80  
FT DISULFID 39 91  
FT DISULFID 57 106  
FT ACT\_SITE 10 10  
FT ACT\_SITE 40 40  
FT ACT\_SITE 113 113  
SQ SEQUENCE 119 AA; 13324 MW; 6072PFB5B7B15BD5A CRC64;

Query Match 24.5%; Score 142; DB 1; Length 119;  
Best Local Similarity 29.8%; Pred. No. 2e-08;  
Matches 34; Conservative 19; Mismatches 45; Indels 16; Gaps 5;

QY 1 QDMVTFQKHLTNRDVDCNNILSTNLF---HCKDKNTFYISRPPEYKATCKGIASKN 56  
1 0NMAKFQEKHRTPTNSNTNCTIMDKSIYIVGGCKERTFTISSATTYKATCSGASTNRN 60  
DB 50 GIATSKNVLTTFE-FYLSDC---NVTSPCKYKLTSTNTEFCVTCENAPVHFV 98  
61 GTHVEDMLYDSNESFDLTDCKNVGCTAPSSCKYNGTGTCKRIIRIACENMGVHF 114

RESULT 6  
ANGR\_MOUSE  
ID ANGR\_MOUSE STANDARD; PRT; 145 AA.

AC Q64438;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Angiogenin-related protein precursor.  
GN ANGRP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Liver;  
RA MEDLINE=96079109; PubMed=8530072;  
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;  
RT "The mouse angiogenin gene family: structures of an angiogenin-related  
protein gene and two pseudogenes.";  
RL Genomics 29:200-206(1995).  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U22519; AAA91367.1; -  
CC HSSP: P03950; 1A4Y.  
DR MGD; MGI:104984; AngRP.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Signal; Hydrolase; Nuclease; Endonuclease.  
FT SIGNAL 1 24  
FT CHAIN 25 145  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 137 137  
FT DISULFID 50 104  
FT DISULFID 63 115  
FT DISULFID 81 130  
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429CAD CRC64;  
Query Match 21.5%; Score 124.5; DB 1; Length 145;  
Best Local Similarity 36.8%; Pred. No. 1.8e-06;  
Matches 28; Conservative 11; Mismatches 30; Indels 7; Gaps 3;  
OY 30 CKDKNTFIYSRPEVKAIC--KGIASKNV-LTTFEFLSDCNVTSR---PCKYKLKKS 82  
DB 63 CKDVTFTIHDTRKNKIKACGKSGSPYGRNLRISKRQVTTCTHKGSRPRPCRYRASKG 122  
OY 83 TNFCVTCENQAPVHF 98  
DB 123 FRYITICENGMPVHF 138  
RESULT 7  
ANGI\_CERAE  
ID ANGI\_CERAE STANDARD; PRT; 146 AA.  
AC Q8WN66;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).  
GN ANG OR RNASE5.  
OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution.";  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOENIN IS ENDOCYTICALLY AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
CC HYDROLYZING CELLULAR tRNAs (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: AF41664; AAL61646.1; -  
DR HydroLase; Nuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 146  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 138 138  
FT DISULFID 50 105  
FT DISULFID 63 116  
FT DISULFID 81 131  
SQ SEQUENCE 146 AA; 16444 MW; 27860112E858BD9 CRC64;  
Query Match 21.5%; Score 124.5; DB 1; Length 146;  
Best Local Similarity 29.7%; Pred. No. 1.8e-06;  
Matches 30; Conservative 17; Mismatches 31; Indels 23; Gaps 4;  
OY 5 TFOKKHLNTRDVCNNILSTNLFCKDKNTFIYSRPEVKAIC--KGIASKNV-LTT 60  
DB 53 TMRRRHLTSP-----CKDINFTHNNHHRKIKGDSGNGNYGENLRISK 97  
OY 61 FEFLSDCNVTS---RPCKYKLKKS TNFCVTCENQAPVH 97  
DB 98 SPFQVTTCTNLGSGSPRPPQYRATRGSRNIVGCENGLPVH 138  
RESULT 8  
RNP\_GALMU  
ID RNP\_GALMU STANDARD; PRT; 124 AA.  
AC P00680;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).  
GN RNASE1 OR RNS1.  
OS Galea musteloides (Cul's).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Galea.  
OX NCBI\_TaxID=10146;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87036770; PubMed=6571219;



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Db 47 DEYCNMAMKRLRPPCKDRNTFTHGNKNKAIKICEDRNCGPYRGLDRISKS-----EFQ 101
Oy 65 LSDC---NVTSR-PCKYKLRKSTNFCVTGCNOAPVHF 98
Db 102 ITICKHKGSSRPPCRGATEDSRIVYGCENGLPVHF 139

RESULT 10
RNPB_CAVPO
ID RNPB_CAVPO STANDARD: PRT: 128 AA.
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
NCBI_Taxid=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77185023; Pubmed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation."
RL Eur. J. Biochem. 75:91-100(1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00826; NRGPB.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT VARIANT 64 64
SQ SEQUENCE 128 AA; 14406 MW; A2FA101A1A33E93B CRC64;

Query Match 20.4%; Score 118; DB 1; Length 128;
Best Local Similarity 25.9%; Pred. No. 7.8e-06;
Matches 30; Conservative 25; Mismatches 39; Indels 22; Gaps 7;

Oy 4 LTFQKHL-----INTRDVDCNNTL--STNLFHCKDKNFTYSRPEYKAIC--KGII 52
Db 6 MKFOGHNDPESPSSNSNY-CNVAMIRNMTCGCKRPVNTFVHESLADYQAVCFQKNVL 64
Oy 53 ASKNVLTFFERY---LSDCNVTSRP---CKYKLRKSTNFCVTGCNO--APVHF 98
Db 65 CKNGQTCYOSYSRMTIDCRVTSSSKFPNCSYRMSQAKSLIVACGEDPVPVPHF 120

RESULT 11
RNP_MYOCO
ID RNP_MYOCO STANDARD: PRT: 128 AA.
AC P00676;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase I) (Rnase A).
GN RNAMEI OR RNSI.
OS Myocastor coypus (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
OC Myocastor.
NCBI_Taxid=10157;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77065676; Pubmed=999896;
RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
RT "Isolation, properties and primary structure of coypu and chinchilla
RT pancreatic ribonuclease."
RL Biochim. Biophys. Acta 453:400-409(1976).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00822; NRCU.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT ACT_SITE 119 119
FT CARBOHYD 34 34
SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 20.2%; Score 117; DB 1; Length 128;
Best Local Similarity 28.2%; Pred. No. 1e-05;
Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;

Oy 6 FQKHL-----INTRDVDCNNTL--STNLF-HCKDKNFTYSRPEYKAICGIIASKNV 57
Db 8 FERQHDHSGSPSTPNPNCNEMKSRMTGCKRPVNTFVHEPLADYQAVC---FQKNV 63
Oy 58 L-----TTFEFLSDCNVTSRP---CKYKLRKSTNFCVTGCNO--APVHF 98
Db 64 LCKNGQTCYOSNSNMHITDCRVTSNSDPNCSYRMSQAKSLIVACGPNVPVPHF 120

RESULT 12
RNP_BALAC
ID RNP_BALAC STANDARD: PRT: 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase I) (Rnase A).
GN RNAMEI OR RNSI.
OS Balaeoptera acutrostrata (Mink whale) (lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeopteridae; Balaeoptera.
NCBI_Taxid=9767;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277855; Pubmed=962870;
RA Emmens M., Wellings G.W., Beintema J.J.;
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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL; AF41667; AAL61649.1; -
CC KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC FT Protein synthesis inhibitor; Signal.
CC FT SIGNAL 1 24 BY SIMILARITY.
CC FT CHAIN 25 146 ANGIOGENIN.
CC FT MOD_RES 25 25 PROLYDINE CARBOXYLIC ACID (BY
CC FT ACT_SITE 37 37 SIMILARITY).
CC FT ACT_SITE 64 64 BY SIMILARITY.
CC FT ACT_SITE 138 138 BY SIMILARITY.
CC FT DISULFD 50 105 BY SIMILARITY.
CC FT DISULFD 63 116 BY SIMILARITY.
CC FT DISULFD 81 131 BY SIMILARITY.
CC SO SEQUENCE 146 AA; E39A89215DB2A2A4 CRC64;
Query Match 19.9%; Score 115.5; DB 1; Length 146;
Best Local Similarity 27.7%; Pred. No. 1.7e+05;
Matches 28; Conservative 17; Mismatches 33; Indels 23; Gaps 4;
OY 5 TFQKKHLNTNRDVDCNNLTSLNLFHCKDKKTFPIYSRPEPKAIC---KGIIASKNV-LTT 60
Db 53 TMRRRHLTSP-----CKDINFVHGNNRHRIITAIIGDEGSGPYGGNLRLST 97
OY 61 FEFYLDPCDNVTS----RPCKYKLKSSTPTFCVCENAPRV 97
Db 98 SPFOYTCKLKGGSPRPCGYTRAIRGSNIIVGCCNGLPVH 138
RESULT 14
ANGI_MOUSE STANDARD: PRT; 145 AA.
AC P21570:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
[2]
RP PARTIAL SEQUENCE.
RC TISSUE=Sera;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiotensin: discernment of functionally important residues and
regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
-1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND,
ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
HYDROLYZING CELLULAR TRNAS.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY
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DR EMBL: U22516; AAA91366.1; -  
DR PIR: A35932; A35932.  
DR HSSP: P03950; 1A4Y.  
DR MGD: MGI:88022; Ang.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
FT Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 145  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 137 137  
FT DISULFID 50 104  
FT DISULFID 63 115  
FT DISULFID 81 130  
SQ SEQUENCE 145 AA; 16228 MW; 06944260DB764938 CRC64;  
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Query Match 19.4%; Score 112.5; DB 1; Length 145;  
Best Local Similarity 34.2%; Pred. No. 3.4e-05;  
Matches 26; Conservative 11; Mismatches 32; Indels 7; Gaps 3;  
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OY 30 CKDKNFTYSPREPKAIC--KGIASKNV-LTTFEFLSDCNVTS---RPCKYKLKKS 82  
DB 63 CKDYNFTFHGKSKAIKICGANGSPYRENLMKSPQVYTKTKGTGSPRPCCYRASAG 122  
OY 83 TMTFCVTCENAPVHF 98  
DB 123 FRHVIVACENGLPVHF 138  
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RESULT 15  
ANGI\_PAPHA  
ID ANGI\_PAPHA STANDARD; PRT: 146 AA.  
AC Q8WNE4;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=9557;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution".  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -!- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY

-----  
CC HYDROLYZING CELLULAR TRNAS (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
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DR EMBL: AF441666; AAU61648.1; -  
DR PIR: A44166; A44166.  
DR HSSP: A44166; A44166.  
DR MGD: MGI:1648; Ang.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
FT Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 146  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 138 138  
FT DISULFID 50 105  
FT DISULFID 63 116  
FT DISULFID 81 131  
SQ SEQUENCE 146 AA; 16432 MW; A4C3CED1482370FE CRC64;  
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Query Match 19.4%; Score 112.5; DB 1; Length 146;  
Best Local Similarity 27.7%; Pred. No. 3.5e-05;  
Matches 28; Conservative 16; Mismatches 34; Indels 23; Gaps 4;  
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OY 5 TFOKKHLTNRDVCNNILSTNLFHCKDKNFTYSPREPKAIC--KGIASKNV-LTT 60  
DB 53 TMRRLHLLSP-----CKDTNFTFHGKSKAIKICGANGSPYRENLMKSPQVYTKTKGTGSPRPCCYRASAG 97  
OY 61 FEFLSDCNV---TSRPCKYKLKKSNTFCVTCENAPVH 97  
DB 98 SPFOVYTKTKLHGSPRPCCYRASAGRNIVGCGENGLPVH 138  
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